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FY632 HTO  
10-30-01  
PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,712A

DATE: 07/05/2001

TIME: 10:42:51

Input Set : A:\37157SEQ.txt

Output Set: N:\CRF3\07052001\I763712A.raw

OCT 12 2001

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3 <110> APPLICANT: Wakamiya, N.  
5 <120> TITLE OF INVENTION: Novel Collectin  
7 <130> FILE REFERENCE: 19036/37157  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/763,712A  
C--> 9 <141> CURRENT FILING DATE: 2001-05-04  
9 <150> PRIOR APPLICATION NUMBER: JP HEI 10-237611  
10 <151> PRIOR FILING DATE: 1998-08-24  
12 <160> NUMBER OF SEQ ID NOS: 32  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 2024  
16 <212> TYPE: DNA  
17 <213> ORGANISM: Homo Sapiens  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (670)..(1695)  
23 <400> SEQUENCE: 1

24 gtcacgaatc tgcagcaaga taccagcggt ctccagggca atctgcagaa ccaaattgtat 60  
25 ttcataatg tggcatcat gaaacctcaac aacctgaacc tgacccagg gcagcagagg 120  
26 aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc 180  
27 aagaacgact ttcaaaatct gcagcagggt tttcttcaag ccaagaagga cacggattgg 240  
28 ctgaaggaga aagtgcagag ctgcagacg ctggctgcca acaactctgc gttggccaaa 300  
29 gccaacaacg acaccctgga gatatgaaac agccagctca actcattcac aggtcagatg 360  
30 gagaacatca ccactatctc tcaagccaaac gaggcagaacc tggaaagaccc gcaggactta 420  
31 cacaagatg cagagaatag aacagccatc aagttaacc aactggagga acgcttccag 480  
32 ctcttgaga cggatattgt gaaatcatc agcaatatca gttacacagc ccaccacctg 540  
33 cggacgctga ccagcaatct aatgaagtc aggaccactt gcacagatac ctttacccaa 600  
34 cacacagatg atctgcaccc ttttgcataat accctggcca acatccgtt ggattctgtt 660  
35 tcttcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta 711  
36 Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val  
37 1 5 10  
38 gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag 759  
39 Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys  
40 15 20 25 30  
41 cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc 807  
42 His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly  
43 35 40 45  
44 ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca 855  
45 Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro  
46 50 55 60  
47 act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct 903  
48 Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro  
49 65 70 75  
50 ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga 951  
51 Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly  
52 80 85 90  
53 gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc 999  
54 Glu Arg Gly Gly Lys Gly Ser Lys Gln Gly Pro Lys Gly Ser

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1047

55	95	100	105	110	
56	cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca				
57	Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro				
58	115	120	125		
59	ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc				1095
60	Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly				
61	130	135	140		
62	cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg				1143
63	Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val				
64	145	150	155		
65	cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca				1191
66	Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro				
67	160	165	170		
68	ggc ccc aag ggc ccc ggc cct cct ggc cca tca gga gcg gtg gtg				1239
69	Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val				
70	175	180	185	190	
71	ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc				1287
72	Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly				
73	195	200	205		
74	tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca				1335
75	Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser				
76	210	215	220		
77	gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag				1383
78	Val Glu Lys Glu Ile Phe Glu Ala Lys Leu Phe Cys Glu Asp Lys				
79	225	230	235		
80	tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata				1431
81	Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile				
82	240	245	250		
83	aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac				1479
84	Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp				
85	255	260	265	270	
86	tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac				1527
87	Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp				
88	275	280	285		
89	tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat				1575
90	Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His				
91	290	295	300		
92	ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac				1623
93	Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn				
94	305	310	315		
95	gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg				1671
96	Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg				
97	320	325	330		
98	gag aca gta ctg tca tct gca tta taacggactg tgatggatc acatgagcaa				1725
99	Glu Thr Val Leu Ser Ser Ala Leu				
100	335	340			
101	attttcagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcatcagat				1785
102	tgaaaaaaaaaaa aaaagcactg aaaaccaatt actaaaaaaaaaattgacacgc tagtgggg				1845
103	taccatccgt cattacccaa agacttggga actaaaatgt tccccagggat gatatgctga				1905

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104 tttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965  
105 atacaaattha tgtctccaa agtatggAAC actccaatca gaaaaaggTT atcatcccg 2024  
107 <210> SEQ ID NO: 2  
108 <211> LENGTH: 547  
109 <212> TYPE: PRT  
110 <213> ORGANISM: Homo Sapiens  
112 <220> FEATURE:  
113 <223> OTHER INFORMATION: Deduced Amino Acid Sequence of Novel Collectin from Nucleotide

114 Sequence  
116 <400> SEQUENCE: 2  
117 Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu  
118 1 5 10 15  
119 Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val  
120 20 25 30  
121 Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn  
122 35 40 45  
123 Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys  
124 50 55 60  
125 Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu  
126 65 70 75 80  
127 Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn  
128 85 90 95  
129 Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn  
130 100 105 110  
131 Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn  
132 115 120 125  
133 Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe  
134 130 135 140  
135 Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His  
136 145 150 155 160  
137 His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys  
138 165 170 175  
139 Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn  
140 180 185 190  
141 Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln  
142 195 200 205  
143 Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val  
144 210 215 220  
145 Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile  
146 225 230 235 240  
147 Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg  
148 245 250 255  
149 Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly  
150 260 265 270  
151 Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu  
152 275 280 285  
153 Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys  
154 290 295 300  
155 Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly

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156 305 310 315 320  
157 Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro  
158 325 330 335  
159 Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln  
160 340 345 350  
161 Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly  
162 355 360 365  
163 Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro  
164 370 375 380  
165 Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln  
166 385 390 395 400  
167 Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp  
168 405 410 415  
169 Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile  
170 420 425 430  
171 Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val  
172 435 440 445  
173 Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val  
174 450 455 460  
175 Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn  
176 465 470 475 480  
177 Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys  
178 485 490 495  
179 Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp  
180 500 505 510  
181 Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu  
182 515 520 525  
183 Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser  
184 530 535 540  
185 Ser Ala Leu  
186 545  
188 <210> SEQ ID NO: 3  
189 <211> LENGTH: 27  
190 <212> TYPE: PRT  
191 <213> ORGANISM: Artificial Sequence  
193 <220> FEATURE:  
194 <223> OTHER INFORMATION: Modified Consensus Sequence of collectins Hybridizable with

Novel

195 Collectin  
197 <400> SEQUENCE: 3  
198 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn  
199 1 5 10 15  
200 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe  
201 20 25  
203 <210> SEQ ID NO: 4  
204 <211> LENGTH: 21  
205 <212> TYPE: DNA  
206 <213> ORGANISM: Artificial Sequence  
208 <220> FEATURE:  
209 <223> OTHER INFORMATION: Sequence of a Reverse Primer for Screening a Novel Collectin.

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211 <400> SEQUENCE: 4  
212 caatctgatg agaagggtgat g 21  
214 <210> SEQ ID NO: 5  
215 <211> LENGTH: 21  
216 <212> TYPE: DNA  
217 <213> ORGANISM: Artificial Sequence  
219 <220> FEATURE:  
220 <223> OTHER INFORMATION: Sequence of a Forward Primer for Screening a Novel Collectin.  
222 <400> SEQUENCE: 5  
223 acgaggggct ggatgggaca t 21  
225 <210> SEQ ID NO: 6  
226 <211> LENGTH: 27  
227 <212> TYPE: PRT  
228 <213> ORGANISM: Artificial Sequence  
230 <220> FEATURE:  
231 <223> OTHER INFORMATION: Consensus sequence of three collectins which were reported heretofore  
232  
234 <400> SEQUENCE: 6  
235 Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro  
236 1 5 10 15  
237 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe  
238 20 25  
240 <210> SEQ ID NO: 7  
241 <211> LENGTH: 24  
242 <212> TYPE: DNA  
243 <213> ORGANISM: Artificial Sequence  
245 <220> FEATURE:  
246 <223> OTHER INFORMATION: M13 Universal Primer Sequence for Sequencing  
248 <400> SEQUENCE: 7  
249 cgacgttgta aaacgacggc cagt 24  
251 <210> SEQ ID NO: 8  
252 <211> LENGTH: 17  
253 <212> TYPE: DNA  
254 <213> ORGANISM: Artificial Sequence  
256 <220> FEATURE:  
257 <223> OTHER INFORMATION: M13 Reverse Primer Sequence for Sequencing.  
259 <400> SEQUENCE: 8  
260 caggaaaca gctatgac 17  
262 <210> SEQ ID NO: 9  
263 <211> LENGTH: 24  
264 <212> TYPE: DNA  
265 <213> ORGANISM: Artificial Sequence  
267 <220> FEATURE:  
268 <223> OTHER INFORMATION: Sequence of a lambda gt11 Reverse Primer for Sequencing.  
270 <400> SEQUENCE: 9  
271 ttgacaccag accaactggt aatg 24  
273 <210> SEQ ID NO: 10  
274 <211> LENGTH: 24  
275 <212> TYPE: DNA

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/763,712A

DATE: 07/05/2001  
TIME: 10:42:52

Input Set : A:\37157SEQ.txt  
Output Set: N:\CRF3\07052001\I763712A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date